

- 1 -

piece 1, NC\_000913, cls\_yciy+, config: linear, direction: +, begin: 1306640, end: 1306831

The diagram illustrates a bacterial promoter region with the following features:

- Transcription Start Sites:** Indicated by arrows pointing left, representing RNA polymerase molecules.
- Regulatory Elements:** Colored boxes representing different regulatory regions. A green box is labeled "sd" (sigma factor binding site). A red box is labeled "ir" (inverted repeat). A blue box is labeled "yciY".
- SD Sequence:** A sequence of nucleotides located upstream of the transcription start site, highlighted in green.
- Inverted Repeat:** A sequence of nucleotides located upstream of the transcription start site, highlighted in red.
- YciY Protein:** A protein binding site located upstream of the transcription start site, highlighted in blue.
- Gap:** A gap between two regulatory elements, indicated by a bracket below the sequence.
- Bit Scores:** Numerical values indicating the strength of each element: "sd-(10)-ir 1306701 Gap 2.7 bits" and "sd-ir 1306701 cls yciY+ total 5.2 bits".

This diagram shows the secondary structure of a ribozyme precursor, likely a 1306800 precursor. The structure is composed of several hairpins and loops. Key features include:

- Exons:** Labeled with green boxes at the top, including \*1306730, \*1306740, \*1306750, \*1306760, \*1306770, \*1306780, \*1306790, and \*1306800.
- Introns:** Shown as red boxes with black dashed lines indicating their boundaries.
- Splice Sites:** Indicated by red dots at the junctions between exons and introns.
- Protein Coding:** Below the sequence, amino acid codons are shown in color-coded boxes: ser-ser-gly-lys-his-leu-alanine-asn-lys-asn-alanine-gly-lys-alanine-leu-val-ser-val-gly-gly-gly-gly-ile-met-thr-ile-leu-leu-leu-his-arg.
- Processing Sites:** Red dots along the backbone indicate where the precursor is processed into mature RNA molecules.
- Regions:** Various regions are highlighted with different colors: blue, orange, yellow, red, and purple.

p35 3.4 bits {-----} sd-(11)-ir 1306779 Gap 3.0 bits |- ... sd

```
{-----} p35-(22)-p10 1306776 Gap 2.3 bits  
|-----| p35-p10 1306776 total 9.4 bits
```

... p35-(23)-p10 1306809 Gap  
p35-p10 1306809 total 4 5

The diagram shows the Val-Lys-Arg-Ser-Arg-Thr peptide sequence. The amino acid sequence is: val - val - arg - met - lys - arg - ser - arg - thr -. Three mutations are indicated by red dots above the sequence at positions 1306810, 1306820, and 1306830. The mutated codons are: \*atg, \*tgc, and \*cgg respectively. The original codons are: agt, aac, and aac.

```
... ----- } sd-(11)-ir 1306812 Gap 3.0 bits  
... ----- | sd-ir 1306812 cls vciY+ total 5.7 bits
```

rd + U rd ir cls\_yciY+

... sd p10 5.6 bits

... ----- } p35-(23)-p10 1306809 Gap 1.4 bits  
... ----- | p35-p10 1306809 total 4.5 bits